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RAW SEQUENCE LISTING

DATE: 03/13/2002

PATENT APPLICATION: US/09/884,814

TIME: 14:25:29

Input Set : A:\-11-1.app

Output Set: N:\CRF3\03132002\I884814.raw

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3 <110> APPLICANT: Chen, Jin-Long
4     Amaral, M. Catherine
5     Tularik Inc.
7 <120> TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
8     Methods of Use
10 <130> FILE REFERENCE: 018781-001110US
12 <140> CURRENT APPLICATION NUMBER: US 09/884,814
13 <141> CURRENT FILING DATE: 2001-06-18
15 <150> PRIOR APPLICATION NUMBER: US 09/124,293
16 <151> PRIOR FILING DATE: 1998-07-29
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 309
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)
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34   20             25             30
35 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
36   35             40             45
37 Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly
38   50             55             60
39 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
40  65             70             75             80
41 Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
42   85             90             95
43 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
44  100            105            110
45 His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
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47 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
48  130            135            140
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50 145            150            155            160
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52 165            170            175
53 Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
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56      195                200                205
57 Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
58      210                215                220
59 Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
60 225                230                235                240
61 Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
62      245                250                255
63 Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
64      260                265                270
65 Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
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78 <220> FEATURE:
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80 <222> LOCATION: (1)..(930)
81 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)
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86 ttacagatcc aaggagaaag tcagggggcca gtgcgcgcta cagccagcgc ccagtaccgc 180
87 ggtgtgatgg gcaccattct gaccatggtg cgtactgagg gccccgaag cctctacaat 240
88 gggctggttg ccggcctgca gcgccaaatg agctttgcct ctgtccgcat cggcctgtat 300
89 gattctgtca aacagttcta caccaagggc tctgagcatg ccagcattgg gagccgcctc 360
90 ctagcaggca gcaccacagg tgccctggct gtggctgtgg ccagcccccac ggatgtggta 420
91 aaggtccgat tccaagctca ggcccgggct ggaggtggtc ggagatacca aagcaccgtc 480
92 aatgcctaca agaccattgc ccgagaggaa gggttccggg gcctctggaa agggacctct 540
93 cccaatgttg ctcgtaatgc cattgtcaac tgtgctgagc tggtgacct a tgacctcatc 600
94 aaggatgccc tctgaaagc caacctcatg acagatgacc tcccttgcca cttcacttct 660
95 gcctttgggg caggcttctg caccactgtc atcgccctcc ctgtagacgt ggtcaagacg 720
96 agatacatga actctgccct gggccagtac agtagcgctg gccactgtgc cttaccatg 780
97 ctccagaagg aggggccccg agccttctac aaagggttca tgccctcctt tctccgcttg 840
98 ggttctctgga acgtggtgat gtctgtcacc tatgagcagc tgaaacgagc cctcatggct 900
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108 <223> OTHER INFORMATION: Description of Artificial Sequence:U1F primer
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131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (1)..(930)
134 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tartaglia et al.
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141 ttt ctt ggg gct ggc aca gct gcc tgc atc gca gat ctc atc acc ttt 96
142 Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe
143 20 25 30
145 cct ctg gat act gct aaa gtc cgg tta cag atc caa gga gaa agt cag 144
146 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
147 35 40 45
149 ggg cca gtg cgc gct aca gtc agc gcc cag tac cgc ggt gtg atg ggc 192
150 Gly Pro Val Arg Ala Thr Val Ser Ala Gln Tyr Arg Gly Val Met Gly
151 50 55 60
153 acc att ctg acc atg gtg cgt act gag ggc ccc cga agc ctc tac aat 240
154 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
155 65 70 75 80
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158 Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
159 85 90 95
161 atc ggc ctg tat gat tct gtc aaa cag ttc tac acc aag ggc tct gag 336
162 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
163 100 105 110
165 cat gcc agc att ggg agc cgc ctc cta gca ggc agc acc aca ggt gcc 384
166 His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
167 115 120 125
169 ctg gct gtg gct gtg gcc cag ccc acg gat gtg gta aag gtc cga ttc 432
170 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
171 130 135 140
173 caa gct cag gcc cgg gct gga ggt ggt cgg aga tac caa agc acc gtc 480
174 Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val
175 145 150 155 160
177 aat gcc tac aag acc att gcc cga gag gaa ggg ttc cgg ggc ctc tgg 528
178 Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp

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179          165          170          175
181 aaa ggg acc tct ccc aat gtt gct cgt aat gcc att gtc aac tgt gct 576
182 Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
183          180          185          190
185 gag ctg gtg acc tat gac ctc atc aag gat gcc ctc ctg aaa gcc aac 624
186 Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
187          195          200          205
189 ctc atg aca gat gac ctc cct tgc cac ttc act tct gcc ttt ggg gca 672
190 Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
191          210          215          220
193 ggc ttc tgc acc act gtc atc gcc tcc cct gta gac gtg gtc aag acg 720
194 Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
195 225          230          235          240
197 aga tac atg aac tct gcc ctg ggc cag tac agt agc gct ggc cac tgt 768
198 Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
199          245          250          255
201 gcc ctt acc atg ctc cag aag gag ggg ccc cga gcc ttc tac aaa ggg 816
202 Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
203          260          265          270
205 ttc atg ccc tcc ttt ctc cgc ttg ggt tcc tgg aac gtg gtg atg ttc 864
206 Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
207          275          280          285
209 gtc acc tat gag cag ctg aaa cga gcc ctc atg gct gcc tgc act tcc 912
210 Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser
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221 <213> ORGANISM: Homo sapiens
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224 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tartaglia et al.
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232 35 40 45
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234 50 55 60
235 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
236 65 70 75 80
237 Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
238 85 90 95
239 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
240 100 105 110

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241 His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
242      115      120      125
243 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
244      130      135      140
245 Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val
246 145      150      155      160
247 Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp
248      165      170      175
249 Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
250      180      185      190
251 Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
252      195      200      205
253 Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
254      210      215      220
255 Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
256 225      230      235      240
257 Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
258      245      250      255
259 Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
260      260      265      270
261 Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
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270 <211> LENGTH: 930
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277 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.
279 <400> SEQUENCE: 7
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281 Met Val Gly Phe Lys Ala Thr Asp Val Pro Pro Thr Ala Thr Val Lys
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285 Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe
286 20 25 30
288 cct ctg gat act gct aaa gtc cgg tta cag atc caa gga gaa agt cag 144
289 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
290 35 40 45
292 ggg cca gtg cgc gct aca gcc agc gcc cag tac cgc ggt gtg atg ggc 192
293 Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly
294 50 55 60
296 acc att ctg acc atg gtg cgt act gag ggc ccc cga agc ctc tac aat 240
297 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn

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VERIFICATION SUMMARY

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DATE: 03/13/2002

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Input Set : A:\-11-1.app

Output Set: N:\CRF3\03132002\I884814.raw

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L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7